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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/978,248

DATE: 11/01/2001  
 TIME: 07:56:29

Input Set : A:\2499-001N.ST25.txt  
 Output Set: N:\CRF3\11012001\I978248.raw

3 <110> APPLICANT: Holland, Pamela M  
 4 Virca, Duke G  
 5 Bird, Timothy A  
 6 Garka, Kristen  
 8 <120> TITLE OF INVENTION: GID (GNK INTERACTING DECARBOXYLASE) AND METHODS OF USE  
 10 <130> FILE REFERENCE: 2499-1-001N  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/978,248 DV  
 13 <141> CURRENT FILING DATE: 2001-10-16  
 15 <150> PRIOR APPLICATION NUMBER: 60/241,324  
 16 <151> PRIOR FILING DATE: 2001-10-18  
 18 <160> NUMBER OF SEQ ID NOS: 27  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 2367  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapien  
 27 <400> SEQUENCE: 1

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32	aagctcatat	ccggagatat	tccaggccca	ctccaggcca	gtgggcaaga	tatggtgagc	180
34	atcctccagt	tagttcagaa	tctcatgcat	ggagatgaag	atgaggagcc	ccagagcccc	240
36	agaatccaaa	atattggaga	acaaggtcat	atggctttgt	tgggacatag	tctgggagct	300
38	tatatattcaa	ctctggacaa	agagaagctg	agaaaaactta	caactaggat	actttcagat	360
40	accaccttat	ggctatgcag	aattttcaga	tatgaaaatg	gggtgtgctta	tttccacgaa	420
42	gaggaaagag	aaggacttgc	aaagatatgt	aggettgcga	ttcattctcg	atatgaagac	480
44	ttcgtagtgg	atggcttcaa	tgtgttatat	aacaagaagc	ctgtcatata	tcttagtgct	540
46	gctgctagac	ctggcctggg	ccaatacctt	tgtaatcagc	tggccttgcc	cttcccctgc	600
48	ttgtgccgtg	tacctgttaa	cactgtgttt	ggatcccagc	atcagatgga	tgttgccctt	660
50	ctggagaaac	tgattaaaga	tgatatagag	cgagggaagac	tgcccctggt	gcttgctgca	720
52	aatgcaggaa	cggcagcagt	aggacacaca	gacaagattg	ggagattgaa	agaactctgt	780
54	gagcagtatg	gcatatggct	tcatgtggag	gggttgaatc	tggcaacatt	ggctctgggt	840
56	tatgtctoct	catcagtgtc	ggctgcagcc	aaatgtgata	gcatgaogat	gactcctggc	900
58	cgtgtgctgg	gtttgccagc	tgttcctgcg	gtgacactgt	ataaacacga	tgacctgccc	960
60	ttgacttttag	ttgctggtct	tacatcaaat	aagcccacag	acaaactccg	tgccctgcct	1020
62	ctgtggttat	ctttacaata	cttgggactt	gatgggtttg	tggagaggat	caagcatgcc	1080
64	tgtcaactga	gtcaacgggt	gcaggaaaag	ttgaagaaaag	tgaattacat	caaaatcttg	1140
66	gtggaagatg	agctcagctc	cccagtggtg	gtgttcagat	ttttccagga	attaccaggc	1200
68	tcagatccgg	tgtttaaagc	cgtcccagtg	cccaacatga	caccttcagg	agtcggccgg	1260
70	gagaggcact	cgtgtgacgc	gctgaatcgc	tggctgggag	aacagctgaa	gcagctgggtg	1320
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74	cctttgatga	cgcagcagct	tttaggaact	cggggagagg	atgtggatca	gctcgtagcc	1440
76	tgcatagaaa	gcaaaactgcc	agtgtctgtc	tgtacgtctc	agttgcgtga	agagtccaag	1500
78	caggaagtgg	aagcaacagc	aggtctccta	tatgttgatg	accctaactg	gtctggaata	1560
80	ggggttgctc	ggtatgaaca	tgctaataat	gataagagca	gtttgaaatc	agatcccga	1620
82	ggggaaaaca	tccatgctgg	actcctgaag	aagttaaatg	aactggaatc	tgacctaac	1680
84	tttaaaatag	gccctgagta	taagagcatg	aagagctgcc	tttatgtcgg	catggcgagc	1740
86	gacaacgtcg	atgtctgtga	gctcgtggag	accattgcgg	ccacagcccg	ggagatagag	1800

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88 gagaactcga ggcttctgga aaacatgaca gaagtgggtc ggaaaggcat tcaggaagct 1860
90 caagtggagc tgcagaaggc aagtgaagaa cggcttctgg aagagggggt gttgcggcag 1920
92 atccctgtag tgggctccgt gctgaattgg ttttctcggg tccaggcttt acagaaggga 1980
94 agaactttta acttgacagc aggtctctctg gagtccacag aacctatata tgtctacaaa 2040
96 gcacaagggtg caggagtcac gctgcctcca acgccctcgg gcagtcgcac caagcagagg 2100
98 cttccaggcc agaagccttt taaaagggtcc ctgcgagggt cagatgcttt gagtgaagacc 2160
100 agctcagtca gtcacattga agacttagaa aaggtggagc gcctatccag tgggcccggag 2220
102 cagatcaccc tgcaggccag cagcactgag ggacaccagc gggctcccag ccctcagcac 2280
104 accgaccaga ccgaggcctt ccagaaaggg gtcccacacc cagaagatga ccactcacag 2340
106 gtagaaggac cggagagctt aagatga 2367
109 <210> SEQ ID NO: 2
110 <211> LENGTH: 788
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapien
114 <400> SEQUENCE: 2
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117 1 5 10 15
120 Gly Lys Asn Leu Lys Glu Ala Val Lys Met Leu Glu Asp Ser Gln Arg
121 20 25 30
124 Arg Thr Glu Glu Glu Asn Gly Lys Lys Leu Ile Ser Gly Asp Ile Pro
125 35 40 45
128 Gly Pro Leu Gln Gly Ser Gly Gln Asp Met Val Ser Ile Leu Gln Leu
129 50 55 60
132 Val Gln Asn Leu Met His Gly Asp Glu Asp Glu Glu Pro Gln Ser Pro
133 65 70 75 80
136 Arg Ile Gln Asn Ile Gly Glu Gln Gly His Met Ala Leu Leu Gly His
137 85 90 95
140 Ser Leu Gly Ala Tyr Ile Ser Thr Leu Asp Lys Glu Lys Leu Arg Lys
141 100 105 110
144 Leu Thr Thr Arg Ile Leu Ser Asp Thr Thr Leu Trp Leu Cys Arg Ile
145 115 120 125
148 Phe Arg Tyr Glu Asn Gly Cys Ala Tyr Phe His Glu Glu Glu Arg Glu
149 130 135 140
152 Gly Leu Ala Lys Ile Cys Arg Leu Ala Ile His Ser Arg Tyr Glu Asp
153 145 150 155 160
156 Phe Val Val Asp Gly Phe Asn Val Leu Tyr Asn Lys Lys Pro Val Ile
157 165 170 175
160 Tyr Leu Ser Ala Ala Ala Arg Pro Gly Leu Gly Gln Tyr Leu Cys Asn
161 180 185 190
164 Gln Leu Gly Leu Pro Phe Pro Cys Leu Cys Arg Val Pro Cys Asn Thr
165 195 200 205
168 Val Phe Gly Ser Gln His Gln Met Asp Val Ala Phe Leu Glu Lys Leu
169 210 215 220
172 Ile Lys Asp Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Leu Val Ala
173 225 230 235 240
176 Asn Ala Gly Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu
177 245 250 255
180 Lys Glu Leu Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val
181 260 265 270

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184 Asn Leu Ala Thr Leu Ala Leu Gly Tyr Val Ser Ser Ser Val Leu Ala
185      275      280      285
188 Ala Ala Lys Cys Asp Ser Met Thr Met Thr Pro Gly Pro Trp Leu Gly
189      290      295      300
192 Leu Pro Ala Val Pro Ala Val Thr Leu Tyr Lys His Asp Asp Pro Ala
193 305      310      315      320
196 Leu Thr Leu Val Ala Gly Leu Thr Ser Asn Lys Pro Thr Asp Lys Leu
197      325      330      335
200 Arg Ala Leu Pro Leu Trp Leu Ser Leu Gln Tyr Leu Gly Leu Asp Gly
201      340      345      350
204 Phe Val Glu Arg Ile Lys His Ala Cys Gln Leu Ser Gln Arg Leu Gln
205      355      360      365
208 Glu Ser Leu Lys Lys Val Asn Tyr Ile Lys Ile Leu Val Glu Asp Glu
209      370      375      380
212 Leu Ser Ser Pro Val Val Val Phe Arg Phe Phe Gln Glu Leu Pro Gly
213 385      390      395      400
216 Ser Asp Pro Val Phe Lys Ala Val Pro Val Pro Asn Met Thr Pro Ser
217      405      410      415
220 Gly Val Gly Arg Glu Arg His Ser Cys Asp Ala Leu Asn Arg Trp Leu
221      420      425      430
224 Gly Glu Gln Leu Lys Gln Leu Val Pro Ala Ser Gly Leu Thr Val Met
225      435      440      445
228 Asp Leu Glu Ala Glu Gly Thr Cys Leu Arg Phe Ser Pro Leu Met Thr
229      450      455      460
232 Ala Ala Val Leu Gly Thr Arg Gly Glu Asp Val Asp Gln Leu Val Ala
233 465      470      475      480
236 Cys Ile Glu Ser Lys Leu Pro Val Leu Cys Cys Thr Leu Gln Leu Arg
237      485      490      495
240 Glu Glu Phe Lys Gln Glu Val Glu Ala Thr Ala Gly Leu Leu Tyr Val
241      500      505      510
244 Asp Asp Pro Asn Trp Ser Gly Ile Gly Val Val Arg Tyr Glu His Ala
245      515      520      525
248 Asn Asp Asp Lys Ser Ser Leu Lys Ser Asp Pro Glu Gly Glu Asn Ile
249      530      535      540
252 His Ala Gly Leu Leu Lys Lys Leu Asn Glu Leu Glu Ser Asp Leu Thr
253 545      550      555      560
256 Phe Lys Ile Gly Pro Glu Tyr Lys Ser Met Lys Ser Cys Leu Tyr Val
257      565      570      575
260 Gly Met Ala Ser Asp Asn Val Asp Ala Ala Glu Leu Val Glu Thr Ile
261      580      585      590
264 Ala Ala Thr Ala Arg Glu Ile Glu Glu Asn Ser Arg Leu Leu Glu Asn
265      595      600      605
268 Met Thr Glu Val Val Arg Lys Gly Ile Gln Glu Ala Gln Val Glu Leu
269      610      615      620
272 Gln Lys Ala Ser Glu Glu Arg Leu Leu Glu Glu Gly Val Leu Arg Gln
273 625      630      635      640
276 Ile Pro Val Val Gly Ser Val Leu Asn Trp Phe Ser Pro Val Gln Ala
277      645      650      655
280 Leu Gln Lys Gly Arg Thr Phe Asn Leu Thr Ala Gly Ser Leu Glu Ser

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281          660          665          670
284 Thr Glu Pro Ile Tyr Val Tyr Lys Ala Gln Gly Ala Gly Val Thr Leu
285          675          680          685
288 Pro Pro Thr Pro Ser Gly Ser Arg Thr Lys Gln Arg Leu Pro Gly Gln
289          690          695          700
292 Lys Pro Phe Lys Arg Ser Leu Arg Gly Ser Asp Ala Leu Ser Glu Thr
293 705          710          715          720
296 Ser Ser Val Ser His Ile Glu Asp Leu Glu Lys Val Glu Arg Leu Ser
297          725          730          735
300 Ser Gly Pro Glu Gln Ile Thr Leu Glu Ala Ser Ser Thr Glu Gly His
301          740          745          750
304 Pro Gly Ala Pro Ser Pro Gln His Thr Asp Gln Thr Glu Ala Phe Gln
305          755          760          765
308 Lys Gly Val Pro His Pro Glu Asp Asp His Ser Gln Val Glu Gly Pro
309          770          775          780
312 Glu Ser Leu Arg
313 785
316 <210> SEQ ID NO: 3
317 <211> LENGTH: 240
318 <212> TYPE: PRT
319 <213> ORGANISM: Periwinkle
321 <400> SEQUENCE: 3
323 Gly Lys Leu Val Cys Tyr Gly Ser Asp Gln Thr His Thr Met Phe Pro
324 1          5          10          15
327 Lys Thr Cys Lys Leu Ala Gly Ile Tyr Pro Asn Asn Ile Arg Leu Ile
328          20          25          30
331 Pro Thr Thr Val Glu Thr Asp Phe Gly Ile Ser Pro Gln Val Leu Arg
332          35          40          45
335 Lys Met Val Glu Asp Asp Val Ala Ala Gly Tyr Val Pro Leu Phe Leu
336          50          55          60
339 Cys Ala Thr Leu Gly Thr Thr Ser Thr Thr Ala Thr Asp Pro Val Asp
340 65          70          75          80
343 Ser Leu Ser Glu Ile Ala Asn Glu Phe Gly Ile Trp Ile His Val Asp
344          85          90          95
347 Ala Ala Tyr Ala Gly Ser Ala Cys Ile Cys Pro Glu Phe Arg His Tyr
348          100          105          110
351 Leu Asp Gly Ile Glu Arg Val Asp Ser Leu Ser Leu Ser Pro His Lys
352          115          120          125
355 Trp Leu Leu Ala Tyr Leu Asp Cys Thr Cys Leu Trp Val Lys Gln Pro
356          130          135          140
359 His Leu Leu Leu Arg Ala Leu Thr Thr Asn Pro Glu Tyr Leu Lys Asn
360 145          150          155          160
363 Lys Gln Ser Asp Leu Asp Lys Val Val Asp Phe Lys Asn Trp Gln Ile
364          165          170          175
367 Ala Thr Gly Arg Lys Phe Arg Ser Leu Lys Leu Trp Leu Ile Leu Arg
368          180          185          190
371 Ser Tyr Gly Val Val Asn Leu Gln Ser His Ile Arg Ser Asp Val Ala
372          195          200          205
375 Met Gly Lys Met Phe Glu Glu Trp Val Arg Ser Asp Ser Arg Phe Glu

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376      210      215      220
379 Ile Val Val Pro Arg Asn Phe Ser Leu Val Cys Phe Arg Leu Lys Pro
380 225      230      235      240
383 <210> SEQ ID NO: 4
384 <211> LENGTH: 240
385 <212> TYPE: PRT
386 <213> ORGANISM: Camptotheca acuminata
388 <400> SEQUENCE: 4
390 His Lys Leu Val Val Tyr Gly Ser Asp Gln Thr His Ser Thr Tyr Ala
391 1      5      10      15
394 Lys Ala Cys Asn Leu Ala Gly Ile Leu Pro Cys Asn Ile Arg Ser Ile
395      20      25      30
398 Arg Thr Glu Ala Val Ala Asn Phe Ser Leu Ser Pro Asp Ser Leu His
399      35      40      45
402 Arg Glu Ile Glu Ala Asp Val Ala Ala Gly Met Val Pro Leu Tyr Leu
403      50      55      60
406 Cys Ala Thr Val Gly Thr Thr Ser Thr Thr Ala Ile Asp Ser Leu Ser
407 65      70      75      80
410 Pro Leu Ala Asp Val Ala Asn Asp Tyr Gly Leu Trp Phe His Val Asp
411      85      90      95
414 Ala Ala Tyr Ala Gly Ser Ala Cys Ile Cys Pro Glu Phe Arg His Tyr
415      100     105     110
418 Leu Asp Gly Ile Glu Arg Ala Asp Ser Leu Ser Leu Ser Pro His Lys
419      115     120     125
422 Trp Leu Leu Ser Tyr Leu Asp Cys Cys Cys Leu Trp Val Lys Arg Pro
423      130     135     140
426 Ser Val Leu Val Lys Ala Leu Ser Thr Asp Pro Glu Tyr Leu Lys Asn
427 145     150     155     160
430 Lys Pro Ser Glu Ser Asn Ser Val Val Asp Phe Lys Asp Trp Gln Val
431      165     170     175
434 Gly Thr Gly Arg Arg Phe Lys Ala Leu Arg Leu Trp Phe Val Met Arg
435      180     185     190
438 Ser Tyr Gly Val Ala Asn Leu Gln Ser His Ile Arg Ser Asp Ile Gln
439      195     200     205
442 Met Ala Lys Met Phe Glu Glu Phe Val Asn Ser Asp Pro Arg Phe Glu
443      210     215     220
446 Ile Val Val Pro Arg Val Phe Ser Leu Val Cys Phe Arg Leu Asn Pro
447 225     230     235     240
450 <210> SEQ ID NO: 5
451 <211> LENGTH: 240
452 <212> TYPE: PRT
453 <213> ORGANISM: Arabidopsis thaliana
455 <400> SEQUENCE: 5
457 Glu Lys Leu Val Val Tyr Ser Ser Asp Gln Thr His Ser Ala Leu Gln
458 1      5      10      15
461 Lys Ala Cys Gln Ile Ala Gly Ile His Pro Glu Asn Cys Arg Val Leu
462      20      25      30
465 Thr Thr Asp Ser Ser Thr Asn Tyr Ala Leu Arg Pro Glu Ser Leu Gln
466      35      40      45

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number